



## Sequence Listing

### (1) GENERAL INFORMATION:

- (i) APPLICANT: Adams, Camilia W.  
Ashkenazi, Avi J.  
Chuntharapai, Anan  
Kim, Kyung J.
  - (ii) TITLE OF INVENTION: Inducing Apoptosis Using Anti-Apo-2 Antibodies
  - (iii) NUMBER OF SEQUENCES: 19
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Genentech, Inc.
    - (B) STREET: 1 DNA Way
    - (C) CITY: South San Francisco
    - (D) STATE: California
    - (E) COUNTRY: USA
    - (F) ZIP: 94080
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: WinPatin (Genentech)
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: US/10/052,798A
    - (B) FILING DATE: 02-NOV-2001
    - (C) CLASSIFICATION:
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 09/079029
    - (B) FILING DATE: 14-MAY-1998
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 60/046615
    - (B) FILING DATE: 15-MAY-1997
  - (vii) PRIOR APPLICATION DATA:
    - (A) APPLICATION NUMBER: 60/074119
    - (B) FILING DATE: 09-FEB-1998
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: Marschang, Diane L.
    - (B) REGISTRATION NUMBER: 35,600
    - (C) REFERENCE/DOCKET NUMBER: P1101R2D1
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: 650/225-5416
    - (B) TELEFAX: 650/952-9881
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 411 amino acids
    - (B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Glu	Gln	Arg	Gly	Gln	Asn	Ala	Pro	Ala	Ala	Ser	Gly	Ala	Arg	
1				5					10					15	
Lys	Arg	His	Gly	Pro	Gly	Pro	Arg	Glu	Ala	Arg	Gly	Ala	Arg	Pro	
				20					25					30	
Gly	Leu	Arg	Val	Pro	Lys	Thr	Leu	Val	Leu	Val	Val	Ala	Ala	Val	
				35					40					45	
Leu	Leu	Leu	Val	Ser	Ala	Glu	Ser	Ala	Leu	Ile	Thr	Gln	Gln	Asp	
				50					55					60	
Leu	Ala	Pro	Gln	Gln	Arg	Ala	Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser	
				65					70					75	
Pro	Ser	Glu	Gly	Leu	Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	
				80					85					90	
Gly	Arg	Asp	Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	
				95					100					105	
His	Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	Asp	
				110					115					120	
Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	Arg	Asn	Thr	
				125					130					135	
Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	Glu	Glu	Asp	Ser	Pro	
				140					145					150	
Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	Gly	Cys	Pro	Arg	Gly	Met	Val	
				155					160					165	
Lys	Val	Gly	Asp	Cys	Thr	Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	
				170					175					180	
Lys	Glu	Ser	Gly	Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	
				185					190					195	
Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
				200					205					210	
Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	Gly	Asp	
				215					220					225	
Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	Ala	Glu	Asp	
				230					235					240	
Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	Gln	Val	
				245					250					255	
Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	
				260					265					270	
Val	Asn	Met	Leu	Ser	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	
				275					280					285	
Ala	Glu	Ala	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	
				290					295					300	

Asn	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	Gln	Cys	Phe	Asp	Asp	
				305					310					315	
Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	Leu	Met	Arg	
				320					325					330	
Lys	Leu	Gly	Leu	Met	Asp	Asn	Glu	Ile	Lys	Val	Ala	Lys	Ala	Glu	
				335					340					345	
Ala	Ala	Gly	His	Arg	Asp	Thr	Leu	Tyr	Thr	Met	Leu	Ile	Lys	Trp	
				350					355					360	
Val	Asn	Lys	Thr	Gly	Arg	Asp	Ala	Ser	Val	His	Thr	Leu	Leu	Asp	
				365					370					375	
Ala	Leu	Glu	Thr	Leu	Gly	Glu	Arg	Leu	Ala	Lys	Gln	Lys	Ile	Glu	
				380					385					390	
Asp	His	Leu	Leu	Ser	Ser	Gly	Lys	Phe	Met	Tyr	Leu	Glu	Gly	Asn	
				395					400					405	
Ala	Asp	Ser	Ala	Xaa	Ser										
				410											

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1799 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCCACGCGTC	CGCATAAATC	AGCACGCGGC	CGGAGAACCC	CGCAATCTCT	50
GCGCCACAA	AATACACCGA	CGATGCCCGA	TCTACTTTAA	GGGCTGAAAC	100
CCACGGGCCT	GAGAGACTAT	AAGAGCGTTC	CCTACCGCC	ATG GAA	145
				Met Glu	
				1	
CAA CGG GGA	CAG AAC GCC	CCG GCC GCT	TCG GGG GCC	CGG	184
Gln Arg Gly	Gln Asn Ala	Pro Ala Ala	Ser Gly Ala	Arg	
	5	10	15		
AAA AGG CAC	GGC CCA GGA	CCC AGG GAG	GCG CGG GGA	GCC	223
Lys Arg His	Gly Pro Gly	Pro Arg Glu	Ala Arg Gly	Ala	
	20	25			
AGG CCT GGG	CTC CGG GTC	CCC AAG ACC	CTT GTG CTC	GTT	262
Arg Pro Gly	Leu Arg Val	Pro Lys Thr	Leu Val Leu	Val	
	30	35	40		
GTC GCC GCG	GTC CTG CTG	TTG GTC TCA	GCT GAG TCT	GCT	301
Val Ala Ala	Val Leu Leu	Val Ser Ala	Glu Ser Ala		
	45	50			
CTG ATC ACC	CAA CAA GAC	CTA GCT CCC	CAG CAG AGA	GCG	340
Leu Ile Thr	Gln Gln Asp	Leu Ala Pro	Gln Gln Arg	Ala	
	55	60	65		

GCC	CCA	CAA	CAA	AAG	AGG	TCC	AGC	CCC	TCA	GAG	GGA	TTG	379
Ala	Pro	Gln	Gln	Lys	Arg	Ser	Ser	Pro	Ser	Glu	Gly	Leu	
	70						75					80	
TGT	CCA	CCT	GGA	CAC	CAT	ATC	TCA	GAA	GAC	GGT	AGA	GAT	418
Cys	Pro	Pro	Gly	His	His	Ile	Ser	Glu	Asp	Gly	Arg	Asp	
			85						90				
TGC	ATC	TCC	TGC	AAA	TAT	GGA	CAG	GAC	TAT	AGC	ACT	CAC	457
Cys	Ile	Ser	Cys	Lys	Tyr	Gly	Gln	Asp	Tyr	Ser	Thr	His	
	95					100					105		
TGG	AAT	GAC	CTC	CTT	TTC	TGC	TTG	CGC	TGC	ACC	AGG	TGT	496
Trp	Asn	Asp	Leu	Leu	Phe	Cys	Leu	Arg	Cys	Thr	Arg	Cys	
			110					115					
GAT	TCA	GGT	GAA	GTG	GAG	CTA	AGT	CCC	TGC	ACC	ACG	ACC	535
Asp	Ser	Gly	Glu	Val	Glu	Leu	Ser	Pro	Cys	Thr	Thr	Thr	
					125					130			
AGA	AAC	ACA	GTG	TGT	CAG	TGC	GAA	GAA	GGC	ACC	TTC	CGG	574
Arg	Asn	Thr	Val	Cys	Gln	Cys	Glu	Glu	Gly	Thr	Phe	Arg	
		135					140					145	
GAA	GAA	GAT	TCT	CCT	GAG	ATG	TGC	CGG	AAG	TGC	CGC	ACA	613
Glu	Glu	Asp	Ser	Pro	Glu	Met	Cys	Arg	Lys	Cys	Arg	Thr	
				150					155				
GGG	TGT	CCC	AGA	GGG	ATG	GTC	AAG	GTC	GGT	GAT	TGT	ACA	652
Gly	Cys	Pro	Arg	Gly	Met	Val	Lys	Val	Gly	Asp	Cys	Thr	
	160					165					170		
CCC	TGG	AGT	GAC	ATC	GAA	TGT	GTC	CAC	AAA	GAA	TCA	GGC	691
Pro	Trp	Ser	Asp	Ile	Glu	Cys	Val	His	Lys	Glu	Ser	Gly	
			175					180					
ATC	ATC	ATA	GGA	GTC	ACA	GTT	GCA	GCC	GTA	GTC	TTG	ATT	730
Ile	Ile	Ile	Gly	Val	Thr	Val	Ala	Ala	Val	Val	Leu	Ile	
	185				190					195			
GTG	GCT	GTG	TTT	GTT	TGC	AAG	TCT	TTA	CTG	TGG	AAG	AAA	769
Val	Ala	Val	Phe	Val	Cys	Lys	Ser	Leu	Leu	Trp	Lys	Lys	
		200					205					210	
GTC	CTT	CCT	TAC	CTG	AAA	GGC	ATC	TGC	TCA	GGT	GGT	GGT	808
Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	Gly	Gly	
				215					220				
GGG	GAC	CCT	GAG	CGT	GTG	GAC	AGA	AGC	TCA	CAA	CGA	CCT	847
Gly	Asp	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	
	225					230					235		
GGG	GCT	GAG	GAC	AAT	GTC	CTC	AAT	GAG	ATC	GTG	AGT	ATC	886
Gly	Ala	Glu	Asp	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	
			240					245					
TTG	CAG	CCC	ACC	CAG	GTC	CCT	GAG	CAG	GAA	ATG	GAA	GTC	925
Leu	Gln	Pro	Thr	Gln	Val	Pro	Glu	Gln	Glu	Met	Glu	Val	
	250				255					260			
CAG	GAG	CCA	GCA	GAG	CCA	ACA	GGT	GTC	AAC	ATG	TTG	TCC	964
Gln	Glu	Pro	Ala	Glu	Pro	Thr	Gly	Val	Asn	Met	Leu	Ser	
		265					270					275	

CCC GGG GAG TCA GAG CAT CTG CTG GAA CCG GCA GAA GCT 1003  
 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala  
 280 285

GAA AGG TCT CAG AGG AGG AGG CTG CTG GTT CCA GCA AAT 1042  
 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn  
 290 295 300

GAA GGT GAT CCC ACT GAG ACT CTG AGA CAG TGC TTC GAT 1081  
 Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp  
 305 310

GAC TTT GCA GAC TTG GTG CCC TTT GAC TCC TGG GAG CCG 1120  
 Asp Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro  
 315 320 325

CTC ATG AGG AAG TTG GGC CTC ATG GAC AAT GAG ATA AAG 1159  
 Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile Lys  
 330 335 340

GTG GCT AAA GCT GAG GCA GCG GGC CAC AGG GAC ACC TTG 1198  
 Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu  
 345 350

TAC ACG ATG CTG ATA AAG TGG GTC AAC AAA ACC GGG CGA 1237  
 Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg  
 355 360 365

GAT GCC TCT GTC CAC ACC CTG CTG GAT GCC TTG GAG ACG 1276  
 Asp Ala Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr  
 370 375

CTG GGA GAG AGA CTT GCC AAG CAG AAG ATT GAG GAC CAC 1315  
 Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu Asp His  
 380 385 390

TTG TTG AGC TCT GGA AAG TTC ATG TAT CTA GAA GGT AAT 1354  
 Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn  
 395 400 405

GCA GAC TCT GCC WTG TCC TAAGTGTG ATTCTCTTCA GGAAGTGAGA 1400  
 Ala Asp Ser Ala Xaa Ser  
 410 411

CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC 1450  
 AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC 1500  
 CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT TTCACTGCAC 1550  
 TTGGCATTAT TTTTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT 1600  
 GTCTGGATCA TTCCGTTTGT GCGTACTTTG AGATTGTGTT TGGGATGTCA 1650  
 TTGTTTTTAC AGCACTTTTT TATCCTAATG TAAATGCTTT ATTTATTTAT 1700  
 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAAA AAAAAAAAAAG 1750  
 GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC 1799

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGAGCCGCT CATGAGGAAG TTGGGCCTCA TGGACAATGA GATAAAGGTG 50  
GCTAAAGCTG AGGCAGCGGG 70

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 930 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATG	ACC	ATG	ATT	ACG	CCA	AGC	TTT	GGA	GCC	TTT	TTT	36	
Met	Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe		
1				5					10				
TTG	GAG	ATT	TTC	AAC	GTG	AAA	AAA	TTA	TTA	TTC	GCA	ATT	75
Leu	Glu	Ile	Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	
	15					20					25		
CCT	TTA	GTT	GTT	CCT	TTC	TAT	GCG	GCC	CAG	CCG	GCC	ATG	114
Pro	Leu	Val	Val	Pro	Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	
				30				35					
GCC	GAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GGA	GGT	GTG	GAA	153
Ala	Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Glu	

40				45				50					
CGG	CCG	GGG	GGG	TCC	CTG	AGA	CTC	TCC	TGT	GCA	GCC	TCT	192
Arg	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	
			55					60					
GGA	TTC	ACC	TTT	GAT	GAT	TAT	GGC	ATG	AGC	TGG	GTC	CGC	231
Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Gly	Met	Ser	Trp	Val	Arg	
65					70					75			
CAA	GCT	CCA	GGG	AAG	GGG	CTG	GAG	TGG	GTC	TCT	GGT	ATT	270
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Gly	Ile	
		80					85					90	
AAT	TGG	AAT	GGT	GGT	AGC	ACA	GGA	TAT	GCA	GAC	TCT	GTG	309
Asn	Trp	Asn	Gly	Gly	Ser	Thr	Gly	Tyr	Ala	Asp	Ser	Val	
				95				100					
AAG	GGC	CGA	GTC	ACC	ATC	TCC	AGA	GAC	AAC	GCC	AAG	AAC	348
Lys	Gly	Arg	Val	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	
105						110					115		
TCC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCC	GAG	GAC	387
Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
			120					125					
ACG	GCC	GTA	TAT	TAC	TGT	GCG	AAA	ATC	CTG	GGT	GCC	GGA	426
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Lys	Ile	Leu	Gly	Ala	Gly	
130					135					140			
CGG	GGC	TGG	TAC	TTC	GAT	CTC	TGG	GGG	AAG	GGG	ACC	ACG	465
Arg	Gly	Trp	Tyr	Phe	Asp	Leu	Trp	Gly	Lys	Gly	Thr	Thr	
		145					150					155	
GTC	ACC	GTC	TCG	AGT	GGT	GGA	GGC	GGT	TCA	GGC	GGA	GGT	504
Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	
				160					165				
GGC	AGC	GGC	GGT	GGC	GGA	TCG	TCT	GAG	CTG	ACT	CAG	GAC	543
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Glu	Leu	Thr	Gln	Asp	
170						175					180		
CCT	GCT	GTG	TCT	GTG	GCC	TTG	GGA	CAG	ACA	GTC	AGG	ATC	582
Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	Val	Arg	Ile	
			185					190					
ACA	TGC	CAA	GGA	GAC	AGC	CTC	AGA	AGC	TAT	TAT	GCA	AGC	621
Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser	
195					200					205			
TGG	TAC	CAG	CAG	AAG	CCA	GGA	CAG	GCC	CCT	GTA	CTT	GTC	660
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	
		210					215					220	
ATC	TAT	GGT	AAA	AAC	AAC	CGG	CCC	TCA	GGG	ATC	CCA	GAC	699
Ile	Tyr	Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	
				225					230				
CGA	TTC	TCT	GGC	TCC	AGC	TCA	GGA	AAC	ACA	GCT	TCC	TTG	738
Arg	Phe	Ser	Gly	Ser	Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	
	235					240					245		
ACC	ATC	ACT	GGG	GCT	CAG	GCG	GAA	GAT	GAG	GCT	GAC	TAT	777

Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr  
 250 255  
 TAC TGT AAC TCC CGG GAC AGC AGT GGT AAC CAT GTG GTA 816  
 Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Val Val  
 260 265 270  
 TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT GCG GCC 855  
 Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala Ala  
 275 280 285  
 GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA AAA 894  
 Ala His His His His His His Gly Ala Ala Glu Gln Lys  
 290 295  
 CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA TAG 930  
 Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
 300 305 309

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 939 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG ACC ATG ATT ACG CCA AGC TTT GGA GCC TTT TTT 36  
 Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe  
 1 5 10  
 TTG GAG ATT TTC AAC GTG AAA AAA TTA TTA TTC GCA ATT 75  
 Leu Glu Ile Phe Asn Val Lys Lys Leu Leu Phe Ala Ile  
 15 20 25  
 CCT TTA GTT GTT CCT TTC TAT GCG GCC CAG CCG GCC ATG 114  
 Pro Leu Val Val Pro Phe Tyr Ala Ala Gln Pro Ala Met  
 30 35  
 GCC GGG GTG CAG CTG GTG GAG TCT GGG GGA GGC TTG GTC 153  
 Ala Gly Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val  
 40 45 50  
 CAG CCT GGG GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT 192  
 Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser  
 55 60  
 GGA TTC ACC TTT AGT AGC TAT TGG ATG AGC TGG GTC CGC 231  
 Gly Phe Thr Phe Ser Ser Tyr Trp Met Ser Trp Val Arg  
 65 70 75  
 CAG GCT CCA GGG AAG GGG CTG GAG TGG GTG GCC AAC ATA 270  
 Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Asn Ile  
 80 85 90  
 AAG CAA GAT GGA AGT GAG AAA TAC TAT GTG GAC TCT GTG 309  
 Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val  
 95 100  
 AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC 348



Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	
105						110					115		
TCA	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCC	GAG	GAC	387
Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
			120					125					
ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	GAT	CTT	TTA	AAG	GTC	426
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Leu	Leu	Lys	Val	
130					135					140			
AAG	GGC	AGC	TCG	TCT	GGG	TGG	TTC	GAC	CCC	TGG	GGG	AGA	465
Lys	Gly	Ser	Ser	Ser	Gly	Trp	Phe	Asp	Pro	Trp	Gly	Arg	
		145					150					155	
GGG	ACC	ACG	GTC	ACC	GTC	TCG	AGT	GGT	GGA	GGC	GGT	TCA	504
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	
				160					165				
GGC	GGA	GGT	GGT	AGC	GGC	GGT	GGC	GGA	TCG	TCT	GAG	CTG	543
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Glu	Leu	
	170					175					180		
ACT	CAG	GAC	CCT	GCT	GTG	TCT	GTG	GCC	TTG	GGA	CAG	ACA	582
Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	
			185					190					
GTC	AGG	ATC	ACA	TGC	CAA	GGA	GAC	AGC	CTC	AGA	AGC	TAT	621
Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	
195					200					205			
TAT	GCA	AGC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	CAG	GCC	CCT	660
Tyr	Ala	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	
		210					215					220	
GTA	CTT	GTC	ATC	TAT	GGT	AAA	AAC	AAC	CGG	CCC	TCA	GGG	699
Val	Leu	Val	Ile	Tyr	Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	
				225					230				
ATC	CCA	GAC	CGA	TTC	TCT	GGC	TCC	AGC	TCA	GGA	AAC	ACA	738
Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser	Gly	Asn	Thr	
	235					240					245		
GCT	TCC	TTG	ACC	ATC	ACT	GGG	GCT	CAG	GCG	GAA	GAT	GAG	777
Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp	Glu	
			250				255						
GCT	GAC	TAT	TAC	TGT	AAC	TCC	CGG	GAC	AGC	AGT	GGT	AAC	816
Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asn	
260					265					270			
CAT	GTG	GTA	TTC	GGC	GGA	GGG	ACC	AAG	CTG	ACC	GTC	CTA	855
His	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	
		275					280					285	
GGT	GCG	GCC	GCA	CAT	CAT	CAT	CAC	CAT	CAC	GGG	GCC	GCA	894
Gly	Ala	Ala	Ala	His	His	His	His	His	His	Gly	Ala	Ala	
				290					295				
GAA	CAA	AAA	CTC	ATC	TCA	GAA	GAG	GAT	CTG	AAT	GGG	GCC	933
Glu	Gln	Lys	Leu	Ile	Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	
	300					305					310		

GCA TAG 939  
Ala  
312

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 933 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG	ACC	ATG	ATT	ACG	CCA	AGC	TTT	GGA	GCC	TTT	TTT	36
Met	Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe	
1				5					10			
TTG	GAG	ATT	TTC	AAC	GTG	AAA	AAA	TTA	TTA	TTC	GCA	ATT 75
Leu	Glu	Ile	Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile
	15					20						25
CCT	TTA	GTT	GTT	CCT	TTC	TAT	GCG	GCC	CAG	CCG	GCC	ATG 114
Pro	Leu	Val	Val	Pro	Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met
				30					35			
GCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GGA	GGC	GTG	GTC 153
Ala	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Gly	Gly	Val	Val
	40					45					50	
CAG	CCT	GGG	CGG	TCC	CTG	AGA	CTC	TCC	TGT	GCA	GCT	TCT 192
Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser
			55					60				
GGG	TTC	ATT	TTC	AGT	AGT	TAT	GGG	ATG	CAC	TGG	GTC	CGC 231
Gly	Phe	Ile	Phe	Ser	Ser	Tyr	Gly	Met	His	Trp	Val	Arg
	65					70				75		
CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG	GCA	GGT	ATT 270
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Gly	Ile
	80						85					90
TTT	TAT	GAT	GGA	GGT	AAT	AAA	TAC	TAT	GCA	GAC	TCC	GTG 309
Phe	Tyr	Asp	Gly	Gly	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
				95					100			
AAG	GGC	CGA	TTC	ACC	ATC	TCC	AGA	GAC	AAT	TCC	AAG	AAC 348
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn
	105					110					115	
ACG	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	GCT	GAG	GAC 387
Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp
			120					125				
ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGA	GAT	AGG	GGC	TAC	TAC 426
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asp	Arg	Gly	Tyr	Tyr
	130				135					140		
TAC	ATG	GAC	GTC	TGG	GGC	AAA	GGG	ACC	ACG	GTC	ACC	GTC 465
Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val
	145					150						155

TCC TCA GGT GGA GGC GGT TCA GGC GGA GGT GGC TCT GGC 504  
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
160 165  
GGT GGC GGA TCG CAG TCT GTG TTG ACG CAG CCG CCC TCA 543  
Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser  
170 175 180  
GTG TCT GGG GCC CCA GGA CAG AGG GTC ACC ATC TCC TGC 582  
Val Ser Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys  
185 190  
ACT GGG AGA AGC TCC AAC ATC GGG GCA GGT CAT GAT GTA 621  
Thr Gly Arg Ser Ser Asn Ile Gly Ala Gly His Asp Val  
195 200 205  
CAC TGG TAC CAG CAA CTT CCA GGA ACA GCC CCC AAA CTC 660  
His Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu  
210 215 220  
CTC ATC TAT GAT GAC AGC AAT CGG CCC TCA GGG GTC CCT 699  
Leu Ile Tyr Asp Asp Ser Asn Arg Pro Ser Gly Val Pro  
225 230  
GAC CGA TTC TCT GGC TCC AGG TCT GGC ACC TCA GCC TCC 738  
Asp Arg Phe Ser Gly Ser Arg Ser Gly Thr Ser Ala Ser  
235 240 245  
CTG GCC ATC ACT GGG CTC CAG GCT GAA GAT GAG GCT GAT 777  
Leu Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp  
250 255  
TAT TAC TGC CAG TCC TAT GAC AGC AGC CTG AGG GGT TCG 816  
Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg Gly Ser  
260 265 270  
GTA TTC GGC GGA GGG ACC AAG GTC ACT GTC CTA GGT GCG 855  
Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala  
275 280 285  
GCC GCA CAT CAT CAT CAC CAT CAC GGG GCC GCA GAA CAA 894  
Ala Ala His His His His His His Gly Ala Ala Glu Gln  
290 295  
AAA CTC ATC TCA GAA GAG GAT CTG AAT GGG GCC GCA 930  
Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
300 305 310  
TAG 933

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 309 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Thr Met Ile Thr Pro Ser Phe Gly Ala Phe Phe Leu Glu Ile  
1 5 10 15  
Phe Asn Val Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro

20										25					30				
Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	Ala	Glu	Val	Gln	Leu	Val	Gln					
				35					40					45					
Ser	Gly	Gly	Gly	Val	Glu	Arg	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser					
				50					55					60					
Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asp	Asp	Tyr	Gly	Met	Ser	Trp					
				65					70					75					
Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser	Gly	Ile					
				80					85					90					
Asn	Trp	Asn	Gly	Gly	Ser	Thr	Gly	Tyr	Ala	Asp	Ser	Val	Lys	Gly					
				95					100					105					
Arg	Val	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu					
				110					115					120					
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys					
				125					130					135					
Ala	Lys	Ile	Leu	Gly	Ala	Gly	Arg	Gly	Trp	Tyr	Phe	Asp	Leu	Trp					
				140					145					150					
Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser					
				155					160					165					
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Glu	Leu	Thr	Gln					
				170					175					180					
Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	Val	Arg	Ile	Thr					
				185					190					195					
Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser	Trp	Tyr	Gln					
				200					205					210					
Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr	Gly	Lys	Asn					
				215					220					225					
Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	Ser					
				230					235					240					
Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp					
				245					250					255					
Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asn	His					
				260					265					270					
Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Ala	Ala					
				275					280					285					
Ala	His	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln	Lys	Leu	Ile					
				290					295					300					
Ser	Glu	Glu	Asp	Leu	Asn	Gly	Ala	Ala											
				305															

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 amino acids

(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe	Leu	Glu	Ile	1	5	10	15
Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro	20	25	30	
Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	Ala	Gly	Val	Gln	Leu	Val	Glu	35	40	45	
Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	50	55	60	
Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Trp	Met	Ser	Trp	65	70	75	
Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Asn	Ile	80	85	90	
Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys	Gly	95	100	105	
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	110	115	120	
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	125	130	135	
Ala	Arg	Asp	Leu	Leu	Lys	Val	Lys	Gly	Ser	Ser	Ser	Gly	Trp	Phe	140	145	150	
Asp	Pro	Trp	Gly	Arg	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	155	160	165	
Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Ser	Glu	170	175	180	
Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	Val	185	190	195	
Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala	Ser	200	205	210	
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr	215	220	225	
Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	230	235	240	
Ser	Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	245	250	255	
Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	260	265	270	
Gly	Asn	His	Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	275	280	285	
Gly	Ala	Ala	Ala	His	His	His	His	His	His	Gly	Ala	Ala	Glu	Gln				

290	295	300
Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala		
305	310	

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 310 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Thr	Met	Ile	Thr	Pro	Ser	Phe	Gly	Ala	Phe	Phe	Leu	Glu	Ile					
1				5				10						15					
Phe	Asn	Val	Lys	Lys	Leu	Leu	Phe	Ala	Ile	Pro	Leu	Val	Val	Pro					
				20				25						30					
Phe	Tyr	Ala	Ala	Gln	Pro	Ala	Met	Ala	Gln	Val	Gln	Leu	Val	Gln					
				35				40						45					
Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser					
				50				55						60					
Cys	Ala	Ala	Ser	Gly	Phe	Ile	Phe	Ser	Ser	Tyr	Gly	Met	His	Trp					
				65				70						75					
Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Gly	Ile					
				80				85						90					
Phe	Tyr	Asp	Gly	Gly	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly					
				95				100						105					
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu					
				110				115						120					
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys					
				125				130						135					
Ala	Arg	Asp	Arg	Gly	Tyr	Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly					
				140				145						150					
Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly					
				155				160						165					
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Ser	Val	Leu	Thr	Gln	Pro	Pro					
				170				175						180					
Ser	Val	Ser	Gly	Ala	Pro	Gly	Gln	Arg	Val	Thr	Ile	Ser	Cys	Thr					
				185				190						195					
Gly	Arg	Ser	Ser	Asn	Ile	Gly	Ala	Gly	His	Asp	Val	His	Trp	Tyr					
				200				205						210					
Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Asp					
				215				220						225					
Ser	Asn	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Arg					
				230				235						240					
Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Thr	Gly	Leu	Gln	Ala	Glu					

	245		250		255
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser Leu Arg					
	260		265		270
Gly Ser Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Ala					
	275		280		285
Ala Ala His His His His His His Gly Ala Ala Glu Gln Lys Leu					
	290		295		300
Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala					
	305		310		

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AGCGGATAAC AATTTACACAGG 23

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTCGTCTTTC CAGACGGTAG T 21

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Ala	Asp	Pro	Asn	Arg	Phe	Arg	Gly	Lys	Asp	Leu
1				5					10		

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe	Ala	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	Leu	Met	Arg
1				5					10					15

Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu  
                   20                                  25                                  30  
 Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp  
                   35                                  40                                  45  
 Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp  
                   50                                  55                                  60  
 Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu  
                   65                                  70                                  75  
 Asp

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Phe Ala Asn Ile Val Pro Phe Asp Ser Trp Asp Gln Leu Met Arg  
   1                                  5                                  10                                  15  
 Gln Leu Asp Leu Thr Lys Asn Glu Ile Asp Val Val Arg Ala Gly  
                   20                                  25                                  30  
 Thr Ala Gly Pro Gly Asp Ala Leu Tyr Ala Met Leu Met Lys Trp  
                   35                                  40                                  45  
 Val Asn Lys Thr Gly Arg Asn Ala Ser Ile His Thr Leu Leu Asp  
                   50                                  55                                  60  
 Ala Leu Glu Arg Met Glu Glu Arg His Ala Lys Glu Lys Ile Gln  
                   65                                  70                                  75  
 Asp

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Val Met Asp Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg  
   1                                  5                                  10                                  15  
 Thr Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val Glu  
                   20                                  25                                  30  
 Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu Lys Arg Trp  
                   35                                  40                                  45  
 Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala Val Tyr Ala Ala Leu  
                   50                                  55                                  60



Glu Arg Met Gly Leu Asp Gly Cys Val Glu Asp Leu Arg Ser  
65 70

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 78 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val	Val	Glu	Asn	Val	Pro	Pro	Leu	Arg	Trp	Lys	Glu	Phe	Val	Arg	
1				5					10					15	
Arg	Leu	Gly	Leu	Ser	Asp	His	Glu	Ile	Asp	Arg	Leu	Glu	Leu	Gln	
				20					25					30	
Asn	Gly	Arg	Cys	Leu	Arg	Glu	Ala	Gln	Tyr	Ser	Met	Leu	Ala	Thr	
				35					40					45	
Trp	Arg	Arg	Arg	Thr	Pro	Arg	Arg	Glu	Ala	Thr	Leu	Glu	Leu	Leu	
				50					55					60	
Gly	Arg	Val	Leu	Arg	Asp	Met	Asp	Leu	Leu	Gly	Cys	Leu	Glu	Asp	
				65					70					75	

Ile Glu Glu

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile	Ala	Gly	Val	Met	Thr	Leu	Ser	Gln	Val	Lys	Gly	Phe	Val	Arg	
1				5					10					15	
Lys	Asn	Gly	Val	Asn	Glu	Ala	Lys	Ile	Asp	Glu	Ile	Lys	Asn	Asp	
				20					25					30	
Asn	Val	Gln	Asp	Thr	Ala	Glu	Gln	Lys	Val	Gln	Leu	Leu	Arg	Asn	
				35					40					45	
Trp	His	Gln	Leu	His	Gly	Lys	Lys	Glu	Ala	Tyr	Asp	Thr	Leu	Ile	
				50					55					60	
Lys	Asp	Leu	Lys	Lys	Ala	Asn	Leu	Cys	Thr	Leu	Ala	Glu	Lys	Ile	
				65					70					75	

Gln Thr